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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/591,632	06/09/2000	Susan Lindquist	27373/34978A	2820

7590 03/13/2006

Marshall O'Toole Gerstein
Murray & Borun
6300 Sears Tower
233 South Wacker Drive
Chicago, IL 60606-6402

EXAMINER

TURNER, SHARON L

ART UNIT	PAPER NUMBER
----------	--------------

1649

DATE MAILED: 03/13/2006

Please find below and/or attached an Office communication concerning this application or proceeding.



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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER

ART UNIT	PAPER
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2-29-06

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

Please see attached Sequence Error Report and Notice to Comply

COUNT SHEET FOR SEQUENCE CASES

Serial No. 05/591,632

AE _____

Date of Count _____

Mark only one space below

X

(CRFN) (CRF is unreadable; use CRF Diskette Problem Report)

(CRFD) (CRF does not comply; use Notice to Comply)

(CRFR) (CRF required but none submitted; use Notice to Comply)

(bona fide) (second or subsequent letter to applicant reporting bona fide attempt to comply; use Notice to Comply and send copy of RSL)

(non bona fide) (second or subsequent letter to applicant reporting non-bona fide attempt to comply; use Notice to Comply and send copy of RSL)

Examiner Sharon L. Turner, Ph.D.

GAU: 1649
1647
1645



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH from the mailing date of this communication within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Turner whose telephone number is (703) 308-0056. If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Gary Kunz whose telephone number is (703) 308-4623. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

SPE is Janet Andrus 571-272-0867

SHARON TURNER, PH.D.
PRIMARY EXAMINER

phone 571-272-0894
2-29-06

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: See attached error report.

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/591,632C
Source: IFW16
Date Processed by STIC: 2/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/591,632C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 J Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:23

Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

3 <110> APPLICANT: Lindquist, et al.
 5 <120> TITLE OF INVENTION: RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS AND
 6 METHODS COMPRISING SAME
 8 <130> FILE REFERENCE: 30554/34978A
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/591,632C
 C--> 10 <141> CURRENT FILING DATE: 2000-06-09
 10 <150> PRIOR APPLICATION NUMBER: US 09/591,632
 11 <151> PRIOR FILING DATE: 2000-06-09
 13 <150> PRIOR APPLICATION NUMBER: US 60/138,833
 14 <151> PRIOR FILING DATE: 1999-06-09
 16 <160> NUMBER OF SEQ ID NOS: 70
 18 <170> SOFTWARE: PatentIn version 3.3

Handwritten notes:
 Use exceeds 72 character
 (see item 2 on Error summary sheet)
 delete - these are not prior data. They are current data.

ERRORED SEQUENCES

429 <210> SEQ ID NO: 3
 430 <211> LENGTH: 1427
 431 <212> TYPE: DNA
 432 <213> ORGANISM: Saccharomyces cerevisiae
 434 <220> FEATURE:
 435 <221> NAME/KEY: CDS
 436 <222> LOCATION: (182)..(1246)
 438 <400> SEQUENCE: 3
 439 ctcgagggttg aaaagaatag caaaaatctt tccttttcaa acagctcatt tggaattggt 60
 441 tatagcactg aattgaaatcg aagaggaata aagatccccc gtacgaactt ctttattttt 120
 443 agtttttcat tttttgttat tagtcatatt gttttaagct gcaaattaag ttgtacacca 180
 445 a atg atg aat aac aac ggc aac caa gtg tcg aat ctc tcc aat gcg ctc 229
 446 Met Met Asn Asn Asn Gly Asn Gln Val Ser Asn Leu Ser Asn Ala Leu
 447 1 5 10 15
 449 cgt caa gta aac ata gga aac agg aac agt aat aca acc acc gat caa 277
 450 Arg Gln Val Asn Ile Gly Asn Arg Asn Ser Asn Thr Thr Thr Asp Gln
 451 20 25 30
 453 agt aat ata aat ttt gaa ttt tca aca ggt gta aat aat aat aat aat 325
 454 Ser Asn Ile Asn Phe Glu Phe Ser Thr Gly Val Asn Asn Asn Asn
 455 35 40 45
 457 aac aat agc agt agt aat aac aat aat gtt caa aac aat aac agc ggc 373
 458 Asn Asn Ser Ser Ser Asn Asn Asn Asn Val Gln Asn Asn Asn Ser Gly
 459 50 55 60
 461 cgc aat ggt agc caa aat aat gat aac gag aat aat atc aag aat acc 421
 462 Arg Asn Gly Ser Gln Asn Asn Asp Asn Glu Asn Asn Ile Lys Asn Thr
 463 65 70 75 80
 465 tta gaa caa cat cga caa caa caa cag gca ttt tcg gat atg agt cac 469

Handwritten notes:
 1426 (p.3)
 Does Not Comply
 Corrected Diskette Needed
 pp 1, 3, 5-6, 7

RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:23

Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

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467					85					90					95		
469	gtg	gag	tat	tcc	aga	att	aca	aaa	ttt	ttt	caa	gaa	caa	cca	ctg	gag	517
470	Val	Glu	Tyr	Ser	Arg	Ile	Thr	Lys	Phe	Phe	Gln	Glu	Gln	Pro	Leu	Glu	
471				100					105					110			
473	gga	tat	acc	ctt	ttc	tct	cac	agg	tct	gcg	cct	aat	gga	ttc	aaa	gtt	565
474	Gly	Tyr	Thr	Leu	Phe	Ser	His	Arg	Ser	Ala	Pro	Asn	Gly	Phe	Lys	Val	
475				115				120					125				
477	gct	ata	gta	cta	agt	gaa	ctt	gga	ttt	cat	tat	aac	aca	atc	ttc	cta	613
478	Ala	Ile	Val	Leu	Ser	Glu	Leu	Gly	Phe	His	Tyr	Asn	Thr	Ile	Phe	Leu	
479		130					135				140						
481	gat	ttc	aat	ctt	ggc	gaa	cat	agg	gcc	ccc	gaa	ttt	gtg	tct	gtg	aac	661
482	Asp	Phe	Asn	Leu	Gly	Glu	His	Arg	Ala	Pro	Glu	Phe	Val	Ser	Val	Asn	
483	145				150				155						160		
485	cct	aat	gca	aga	gtt	cca	gct	tta	atc	gat	cat	ggg	atg	gac	aac	ttg	709
486	Pro	Asn	Ala	Arg	Val	Pro	Ala	Leu	Ile	Asp	His	Gly	Met	Asp	Asn	Leu	
487				165				170				175					
489	tct	att	tgg	gaa	tca	ggg	gcg	att	tta	tta	cat	ttg	gta	aat	aaa	tat	757
490	Ser	Ile	Trp	Glu	Ser	Gly	Ala	Ile	Leu	Leu	His	Leu	Val	Asn	Lys	Tyr	
491				180				185				190					
493	tac	aaa	gag	act	ggg	aat	cca	tta	ctc	tgg	tcc	gat	gat	tta	gct	gac	805
494	Tyr	Lys	Glu	Thr	Gly	Asn	Pro	Leu	Leu	Trp	Ser	Asp	Asp	Leu	Ala	Asp	
495		195					200				205						
497	caa	tca	caa	atc	aac	gca	tgg	ttg	ttc	ttc	caa	acg	tca	ggg	cat	gcg	853
498	Gln	Ser	Gln	Ile	Asn	Ala	Trp	Leu	Phe	Phe	Gln	Thr	Ser	Gly	His	Ala	
499		210				215					220						
501	cca	atg	att	gga	caa	gct	tta	cat	ttc	aga	tac	ttc	cat	tca	caa	aag	901
502	Pro	Met	Ile	Gly	Gln	Ala	Leu	His	Phe	Arg	Tyr	Phe	His	Ser	Gln	Lys	
503	225				230				235					240			
505	ata	gca	agt	gct	gta	gaa	aga	tat	acg	gat	gag	gtt	aga	aga	gtt	tac	949
506	Ile	Ala	Ser	Ala	Val	Glu	Arg	Tyr	Thr	Asp	Glu	Val	Arg	Arg	Val	Tyr	
507				245				250				255					
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510	Gly	Val	Val	Glu	Met	Ala	Leu	Ala	Glu	Arg	Arg	Glu	Ala	Leu	Val	Met	
511				260				265				270					
513	gaa	tta	gac	acg	gaa	aat	gag	gct	gca	tac	tca	gct	ggg	aca	aca	cca	1045
514	Glu	Leu	Asp	Thr	Glu	Asn	Ala	Ala	Ala	Tyr	Ser	Ala	Gly	Thr	Thr	Pro	
515		275					280				285						
517	atg	tca	caa	agt	cgt	ttc	ttt	gat	tat	ccc	gta	tgg	ctt	gta	gga	gat	1093
518	Met	Ser	Gln	Ser	Arg	Phe	Phe	Asp	Tyr	Pro	Val	Trp	Leu	Val	Gly	Asp	
519		290				295					300						
521	aaa	tta	act	ata	gca	gat	ttg	gcc	ttt	gtc	cca	tgg	aat	aat	gtc	gtg	1141
522	Lys	Leu	Thr	Ile	Ala	Asp	Leu	Ala	Phe	Val	Pro	Trp	Asn	Asn	Val	Val	
523	305				310				315					320			
525	gat	aga	att	ggc	att	aat	atc	aaa	att	gaa	ttt	cca	gaa	gtt	tac	aaa	1189
526	Asp	Arg	Ile	Gly	Ile	Asn	Ile	Lys	Ile	Glu	Phe	Pro	Glu	Val	Tyr	Lys	
527				325				330				335					
529	tgg	acg	aag	cat	atg	atg	aga	aga	ccc	gag	gtc	atc	aag	gca	ttg	cgt	1237
530	Trp	Thr	Lys	His	Met	Met	Arg	Arg	Pro	Ala	Val	Ile	Lys	Ala	Leu	Arg	

RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:23

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Output Set: N:\CRF4\02072006\I591632C.raw

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533 ggt gga tga aggctgcttt aaaaacaaga aagaaagaag aaggaggaaa      1286
534 Gly Gly
537 agaagggttat aagggtatgt atataggcag acaaaaagga aaattaagtg caaatataaa      1346
539 caaaaatgtc atagaagtat ataatagttt tgaaatttct gttgcttcta tttattcttt      1406
E--> 541 gttaccccaa ccacagaatt      1427/1426
724 <210> SEQ ID NO: 11
725 <211> LENGTH: 446 445
726 <212> TYPE: DNA
727 <213> ORGANISM: Artificial sequence
729 <220> FEATURE:
730 <223> OTHER INFORMATION: CUP1 promoter
732 <400> SEQUENCE: 11
733 ccattaccga catttggcg ctatacgtgc atatgttcat gtatgtatct gtatttaaaa      60
735 cacttttgta ttatttttcc tcatatatgt gtataggttt atacggatga ttaattatt      120
737 acttcaccac cttttatttc aggtgatata cttagccttg ttactagtta gaaaaagaca      180
739 tttttgctgt cagtcactgt caagagattc ttttgcgtgc atttcttcta gaagcaaaaa      240
741 gagcgatgcg tcttttccgc tgaaccgttc cagcaaaaaa gactaccaac gcaatatgga      300
743 ttgtcagaat catataaaaag aagaagcaaa taactccttg tcttgatca attgcattat      360
745 atatcttctt gttagtgcaa tatcatatag aagtcacga aatagatatt aagaaaaaca      420
E--> 747 aactgtacaa tcaatcaatc aatca      445
3712 <210> SEQ ID NO: 45
3713 <211> LENGTH: 7239 7238 (pg 5-6)
3714 <212> TYPE: DNA
3715 <213> ORGANISM: Artificial sequence
3717 <220> FEATURE:
3718 <223> OTHER INFORMATION: Vector containing chimeric gene
3720 <400> SEQUENCE: 45
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3723 cttaggacgg atcgcttgcc tgaacttac acgcgcctcg tatcttttaa tgatggaata      120
3725 atttgggaat ttactctgtg tttattttat ttatgtttt gtatttggat tttagaaagt      180
3727 aaataaagaa ggtagaagag ttacggaatg aagaaaaaaa aataaacaaa ggtttaaaaa      240
3729 atttcaacaa aaagcgtact ttacatatat atttattaga caagaaaagc agattaaata      300
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3741 ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg      660
3743 ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt      720
3745 attcaacatt tccgtgtcgc ccttattccc tttttgctcg cattttgcct tctgttttt      780
3747 gctcaccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagt      840
3749 ggttacatcg aactggtatc caacagcggg aagatccttg agagttttcg ccccgagaa      900
3751 cgttttccaa tgatgagcac ttttaagtt ctgctatgtg gcgcggtatt atcccgatt      960
3753 gacgcggggc aagagcaact cggtcgcgcg atacactatt ctcaaatga cttggttgag      1020
3755 tactcaccag tcacagaaaa gcatcttacg gatggcatga cagtaagaga attatgcagt      1080
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3759 ccgaaggagc taaccgcttt tttgcacaac atgggggagc atgtaactcg ccttgatcgt      1200
3761 tgggaaccgg agctgaatga agccatacca aacgacgagc gtgacaccac gatgcctgta      1260

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RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:23

Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

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3771	gggagtcagg	caactatgga	tgaacgaaat	agacagatcg	ctgagatagg	tgccctcactg	1560
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3775	cttcattttt	aatttaaaaag	gatctagggtg	aagatccctt	ttgataatct	catgacccaaa	1680
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3779	tcttcttgag	atcctttttt	tctgcgcgta	atctgctgct	tgcaaaacaaa	aaaaccaccg	1800
3781	ctaccagcgg	tggtttggtt	gccggatcaa	gagctaccaa	ctctttttcc	gaaggtaact	1860
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3785	cacttcaaga	actctgtagc	accgcctaca	tacctcgctc	tgctaatect	gttaccagtg	1980
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3797	tgacttgagc	gtcgattttt	gtgatgctcg	tcaggggggc	ggagcctatg	gaaaaacgcc	2340
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3815	gataagcttg	atatcgaaat	cccattaccg	acatttgggc	gctatacgtg	catatgttca	2880
3817	tgtatgtatc	tgtatttaaa	acacttttgt	attatttttc	ctcatatatg	tgtataggtt	2940
3819	tatacggatg	atttaattat	tacttcacca	ccctttatct	caggctgata	tcttagcctt	3000
3821	gttactagtt	agaaaaagac	atttttgctg	tcagtcaetg	tcaagagatt	cttttgctgg	3060
3823	catttcttct	agaagcaaaa	agagcgtatg	gtcttttccg	ctgaaccgtt	ccagcaaaaa	3120
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3827	tcttgtatca	attgcattat	aatatcttct	tgttagtgca	atatcatata	gaagtcacgc	3240
3829	aaatagatat	taagaaaaac	aaactgtaca	atcaatcaat	caatcaggat	ccatggatac	3300
3831	ggataagtta	atctcagagg	ctgagttctca	tttttctcaa	ggaaaccatg	cagaagctgt	3360
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3839	taaggggttct	tcccaaacgc	aactaggaaa	actagctttg	ttagccacag	tgatgacaca	3600
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3857	tgggtggtgct	ttttcctcat	tggcctccat	ggctcaatct	tacttaggtg	gtggacaaac	4140
3859	tcaatccaac	caacagcaat	acaatcaaca	aggccaaaac	aaccagcagc	aataccagca	4200

RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:23

Input Set : A:\34978a.txt

Output Set : N:\CRF4\02072006\I591632C.raw

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humbler
 ff

RAW SEQUENCE LISTING

DATE: 02/07/2006

PATENT APPLICATION: US/09/591,632C

TIME: 09:01:23

Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

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7200
7239

hos.
off

from sequence 39

09/591, 632C

7

gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa tga 720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp glu Leu Tyr Lys
225 230 235

(240) delete, since
no amend
sent
is shown

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/591,632C

DATE: 02/07/2006

TIME: 09:01:24

Input Set : A:\34978a.txt

Output Set: N:\CRF4\02072006\I591632C.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:541 M:254 E: No. of Bases conflict, LENGTH:Input:1427 Counted:1426 SEQ:3
L:541 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1427 Found:1426 SEQ:3
L:747 M:252 E: No. of Seq. differs, <211> LENGTH:Input:446 Found:445 SEQ:11
L:3593 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:39
L:3869 M:254 E: No. of Bases conflict, LENGTH:Input:4500 Counted:4499 SEQ:45
M:254 Repeated in SeqNo=45
L:3961 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7239 Found:7238 SEQ:45